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OM nucleic - nucleic search, using sw model

Run on: November 30, 2002, 10:11:38 ; Search time 77 Seconds

(without alignments) 11016.467 Million cell updates/sec

Sequence: 1 atggcgtgtttaaagtgcac... gctcatatcaagggttctaa 2766
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gabext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database: 1. Issued Patents/NA: *
1: /egn2_6/ptodata/1/ina5A_COMB.seq: *
2: /egn2_6/ptodata/1/ina6A_COMB.seq: *
3: /egn2_6/ptodata/1/ina6B_COMB.seq: *
4: /egn2_6/ptodata/1/ina6C_COMB.seq: *
5: /egn2_6/ptodata/1/ina6D_COMB.seq: *
6: /egn2_6/ptodata/1/ina6E_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
c 1	78.8	2.8	7218 1	US-08-232-463-14
c 2	51.6	1.9	7218 1	US-08-232-463-14
c 3	50.2	1.8	390 4	US-09-197-649-7
c 4	44.2	1.6	4403765 4	US-09-103-840-2
c 5	40.2	1.5	1174 3	US-09-034-985-1
c 6	39.6	1.4	3431 4	US-09-221-017B-993
c 7	39	1.4	1926 4	US-09-240-588A-4
c 8	39	1.4	1931 2	US-09-130-114-2
c 9	38.6	1.4	1548 2	US-08-762-106-5
c 10	38.6	1.4	1548 4	US-09-320-774-5
c 11	38.6	1.4	1581 2	US-08-762-106-6
c 12	38.6	1.4	1581 4	US-09-320-774-6
c 13	38.4	1.4	2777 4	US-09-310-463-3
c 14	38.4	1.4	2777 4	US-08-842-248A-3
c 15	38.4	1.4	50937 4	US-09-428-517-1
c 16	38.2	1.4	289 4	US-09-007-005-17
c 17	38.2	1.4	289 4	US-09-241-796-17
c 18	37.4	1.4	1734 6	5352575
c 19	37	1.3	1890 3	US-08-935-855-19
c 20	37	1.3	2194 2	US-08-942-569A-9
c 21	37	1.3	2194 2	US-09-188-469-9
c 22	37	1.3	2194 4	US-09-972-238A-9
c 23	36.8	1.3	2790 3	US-08-985-950-21
c 24	35.8	1.3	2922 4	US-09-310-461-1
c 25	35.8	1.3	2922 4	US-08-842-248A-1
c 26	36.6	1.3	289 4	US-09-005-17
c 27	1.3	289 4	US-09-244-796-17	

ALIGNMENTS

RESULT 1
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHETTLINGER, F.
; APPLICANT: PALKNER, F.G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Hardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REFERENCE/DOCKET NUMBER: 29 768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEFAX: (703)836-9300
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pIZgpt-F1s
; US-08-232-463-14

Query Match 2.8% ; Score 78.8; DB 1; Length 7218;

Best Local Similarity 3.8%; Pred. No. 4.4e-12; Mismatches 14; Conservative 231; Mismatches 123; Indels 0; Gaps 0; Matches 14

TYPE: nucleic acid
STRANDBEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pZP9pt-F1s
US-08-232-463-14

Query Match 1.9%; Score 51.6; DB 1; Length 7218;
Best Local Similarity 5.9%; Pred. No. 0.00027; Mismatches 169; Indels 0; Gaps 0; Matches 24; Conservative 215; Mismatches 169; Indels 0; Gaps 0; Matches 24

QY 395 CTGCTCTCAACCTGACCCCTATGCCCTGGGTCCTGCTCTGAGATACTCTCTCTT 454
Db 1078 VYY 1137
QY 455 TAATTGGGTGTGGGTCATGGGTTCATGTCGTTGATCTGGACCTCTACATTGTTAG 514
Db 1138 VYY 1197
QY 515 GGAGTCAGCCTCAACATGTTCTATCATCATGTCATCTGTCAGCTGATCCAGACG 574
Db 1198 VYY 1257
QY 575 GAGAGACTCGCAAGATAGCATCTAGAGTCAGACTACGGGACAACTGATCAAG 2037
Db 1258 VYY 1317
QY 635 TGGCTCATCTGGCTATATGATTCTGGCACTCTCTCCCTGGTGTGGTCAGGTT 694
Db 1318 VYY 1377
QY 695 GGGAGGCCCTCCACTCTCTCTCTCTCTCCAGTGTGTCCTCTGGTGTGGCAGAG 802
Db 1378 VYYGTA 1437
QY 755 ATAAACCACTGCCTCTTACAATACATGACACAAAGTACCGCACAG 1485
Db 1438 CCAAATCTCTCATCTTAACTACTGTGATAGATAGTAATTACAG

RESULT 2
US-08-232-463-14

Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:

APPLICANT: DORNER, F.
APPLICANT: SCHETTLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,463
FILING DATE: 26-AUG-1991
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)356-9300
TELEFAX: (703)683-4109
TELE: 899149

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

Query Match 1.8%; Score 50.2; DB 4; Length 390;

RESULT 3
US-09-197-649-7/C

Sequence 7, Application US/09197649
Patent No. 6194550
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Turk, Craig
APPLICANT: Pribnow, David
APPLICANT: Smith, Jonathon D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEX02/CL-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1988-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1982-01-31
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER FILING DATE: 1981-08-01
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1980-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 390
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: having a 120 repeat of ACC flanked by fixed
OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

us-09-130-114-2
 Sequence 2, Application US/09130114
 Patent No. 5976807
 GENERAL INFORMATION:
 APPLICANT: Horlick, Robert A.
 APPLICANT: Demaj, Bassam B.
 APPLICANT: Robbins, Alan K.
 TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
 FILE REFERENCE: 0667/1990JUSL
 CURRENT APPLICATION NUMBER: US/09/130,114
 CURRENT FILING DATE: 1998-08-06
 NUMBER OF SEQ ID NOS: 36
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 1931
 TYPE: DNA
 ORGANISM: E. coli
 US-09-130-114-2

Query Match 1.4%; Score 39; DB 2; Length 1931;

Best Local Similarity 44.2%; Pred. No. 0.51; Mismatches 0; Indels 3; Gaps 1; Matches 208; Conservative 0; Mismatches 260; Indels 3; Gaps 1;

Qy 2172 CGTCATGCCACTTCTGACTGTCCTCGAGGTGCGTTGGCTGTGTGCCCGACAGA 2231
 Db 550 CGTCCTCGTCGCCCTCCCGCTCCCGCTCCCGTCCTCGTCCTCCCGCTCC 609
 Qy 2232 GRACTGCCACGGCTGGGCCCTGGCTCGCCGTCATCCTCATGCACTGTCACCGC 2291
 Db 610 CGTCCTCCCGCTCCCGCTCCCGTCCTCCCGTCCTCGTCCTCCCGCTCC 669
 Qy 2292 CATCATGGGACCTGGCGACTGGCGCTGCACTTGCGCTGCAAGATTCAGTCAC 2351
 Db 670 CGTCCTCCCGCTCCCGCTCCCGTCCTCGTCCTCCCGCTCCCGCTCC 729
 Qy 2352 AGCTGTTGTTGTTGGCATTTGGACACTCTGGTCCAGATAGTTTCCACAGCTGC 2411
 Db 730 CCCGTCCTCGTCCTCC--CGTCCTCCCGTCCTCGTCCTCCCGTCCTCC 786
 Qy 2412 TGCCTCTCAGGAGTATATGGACAGACGGCTCCATGGAAACGGTACGGGACGGCAACCGGT 2471
 Db 787 CGTCCTCCGGCTCCGGTCCTCCGGTCCTCCGGTCCTCCGGTCCTCCGGTCCTCC 846
 Qy 2472 CAAATGTTCCGGCATCGGACCTGGCGGCGACACTGGCTTCGGTACCCCTTCAACAT 2531
 Db 847 CCCGGTCTCCCGTCCTCCGGTCCTCCGGTCCTCCGGTCCTCCGGTCCTCC 906
 Qy 2532 GGGACAGGAGTTCGAGTGTGGCGGCCACACTGGCTTCGGTACCCCTTCAACAT 2591
 Db 907 CGTCCTCGTCCTCCCGTCCTCCGGTCCTCCGGTCCTCCGGTCCTCCGGTCCTCC 966
 Qy 2592 CTTGCAATTGTCGATCAGGGTCTCTGACCGGACCT 2642
 Db 967 CCTCGTCTCCACCTGGGCCAGCTCCGGTCACCTCGGCCAGCT 1017

RESULT 10
 US-09-220-774-5/c
 Sequence 5, Application US/09320774
 Patent No. 6265545
 GENERAL INFORMATION:
 APPLICANT: JARVIK, Jonathan W.
 TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
 TITLE OF INVENTION: TAGGING
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Harris Brotnan
 STREET: 202 Coast Blvd., Suite 111
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/320,774
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/762,106
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brotnan, Harris F.
 REGISTRATION NUMBER: 35,461

RESULT 9
 US-08-762-106-5/c
 Sequence 5, Application US/08762106
 Patent No. 5948677
 GENERAL INFORMATION:
 APPLICANT: Jarvik, Jonathan W.
 TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
 TITLE OF INVENTION: TAGGING
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Harris Brotnan
 STREET: 202 Coast Blvd., Suite 111
 CITY: La Jolla
 STATE: California
 COUNTRY: US
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/320,774
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/762,106
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Brotnan, Harris F.
 REGISTRATION NUMBER: 35,461

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 654-2428
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1548 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-320-774-5

Query Match 1.4%; Score 38.6; DB 4; Length 1548;
 Best Local Similarity 52.9%; Pred. No. 0.59; Matches 83; Conservative 0; Mismatches 74; Indels 0; Gaps 0; Gaps 0; Length 1548; Db 1086 CACGCCCTCAGCTCTTCCTTGAGCTCCGCTCAGTCCTGGCCCTCGGCCA 1027

Qy 2436 CGCTCCATTGGCAACGAGACGGCAGCACCGCGTCAATGTCCTGGCATCGGCC 2495
 Db 1086 CACGCCCTCAGCTCTTCCTTGAGCTCCGCTCAGTCCTGGCCCTCGGCCA 1027

Qy 2496 GGCTGGTCGAGGCCGACATCTACTGGCTCTGAGACAGAGGTCACGTCGGC 2555
 Db 1026 GGCTCCACAGTGACGCCGGCTGCGCCCTGTCCCGCAGGGTGCCTGCGATGGCTG 967

Qy 2556 CGGACACTGGCTCTCGTCACCCCTTCACATC 2592
 Db 966 CAGGCCGCCGCCGCTCCACCAAGCTGTCCACC 930

RESULT 11
 US-08-762-106-6/C
 Sequence 6, Application US/08762106
 ; PATENT NO. 5948677
 ; GENERAL INFORMATION:
 ; APPLICANT: Jarvik, Jonathan W.
 ; TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
 ; NUMBER OF SEQUENCES: 47
 ; ADDRESSEE: Harris Brotnan
 ; STREET: 202 Coast Blvd., Suite 111
 ; CITY: La Jolla
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/320.774
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/762,106
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brotnan, Harris F.
 ; REGISTRATION NUMBER: 35,461
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 654-2428
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1581 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-09-320-774-6

Query Match 1.4%; Score 38.6; DB 4; Length 1581;
 Best Local Similarity 52.9%; Pred. No. 0.6; Matches 83; Conservative 0; Mismatches 74; Indels 0; Gaps 0; Gaps 0; Length 1581; Db 1086 CACGCCCTCAGCTCTTCCTTGAGCTCCGCTCAGTCCTGGCCCTCGGCCA 1027

Qy 2436 CGCTCCATTGGCAACGAGACGGCAGCACCGCGTCAATGTCCTGGCATCGGCC 2495
 Db 1086 CACGCCCTCAGCTCTTCCTTGAGCTCCGCTCAGTCCTGGCCCTCGGCCA 1027

Qy 2496 GGCTGGTCGAGGCCGACATCTACTGGCTCTGAGACAGAGGTCACGTCGGC 2555
 Db 1026 GGCTCCACAGTGACGCCGGCTGCGCCCTGTCCCGCAGGGTGCCTGCGATGGCTG 967

Qy 2556 CGGACACTGGCTCTCGTCACCCCTTCACATC 2592
 Db 966 CAGGCCGCCGCCGCTCCACCAAGCTGTCCACC 930

RESULT 12
 US-09-320-774-6/C
 Sequence 6, Application US/09320774
 ; PATENT NO. 626545
 ; GENERAL INFORMATION:
 ; APPLICANT: Jarvik, Jonathan W.
 ; TITLE OF INVENTION: READING FRAME INDEPENDENT EPITOPE
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Harris Brotnan
 ; STREET: 202 Coast Blvd., Suite 111
 ; CITY: La Jolla
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/320.774
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/762,106
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brotnan, Harris F.
 ; REGISTRATION NUMBER: 35,461
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 654-2428
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1581 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-09-320-774-6

Query Match 1.4%; Score 38.6; DB 4; Length 1581;
 Best Local Similarity 52.9%; Pred. No. 0.6; Matches 83; Conservative 0; Mismatches 74; Indels 0; Gaps 0; Gaps 0; Length 1581; Db 1086 CACGCCCTCAGCTCTTCCTTGAGCTCCGCTCAGTCCTGGCCCTCGGCCA 1027

Qy 2436 CGCTCCATTGGCAACGAGACGGCAGCACCGCGTCAATGTCCTGGCATCGGCC 2495
 Db 1086 CACGCCCTCAGCTCTTCCTTGAGCTCCGCTCAGTCCTGGCCCTCGGCCA 1027

Qy 2496 GGCTGGTCGAGGCCGACATCTACTGGCTCTGAGACAGAGGTCACGTCGGC 2555
 Db 1026 GGCTCCACAGTGACGCCGGCTGCGCCCTGTCCCGCAGGGTGCCTGCGATGGCTG 967

Qy 2556 CGGACACTGGCTCTCGTCACCCCTTCACATC 2592
 Db 966 CAGGCCGCCGCCGCTCCACCAAGCTGTCCACC 930

Best Local Similarity 47.8%; Pred. No. 4.9;
Matches 111; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
Qy 2049 GGCCTGGTGGGGGACCATTCCTGGAGGGGACAGTCATGGGCATACCGTCAG 2108
Db 595 GGACCTACCCGGGGCAGGACCCACGCCGCGAGGGCGCCACCGGGCG 654
Qy 2109 TGCAGCAGGGTGGAGGATGAGATGAAATCCGGGAGGAGGCTGCCCTCCCTTGA 2168
Db 655 GGGGACCGGGGAGCAGGGAGGGAGGGAGGGAGGGAGGGAGGGCTGGAGGCTAC 714
Qy 2169 CTACCTCATGCCACCTGACTGACTGTTCTCTGGAAGGTGCTTGTGTTCTGTCGCCCCAAC 2228
Db 715 CCGGCTCTGGCTCTCTGGAGGAGCACCGGGGAGCACCCGGCCACCGAGTCCTCAT 774
Qy 2229 AGAGTACTGCCACGCTGGCCCTTCCCGCTCCATCTCATCATGCG 2280
Db 775 CGGCCCCAACCGCTGCACTGTCGCTGGCCACCTTCCAGATCAGGGC 826

Search completed: November 30, 2002, 13:01:06
Total time : 2282 secs